ORIGINAL ARTICLE

Mapping the quantitative trait loci (QTL) for body shape and conformation measurements on BTA1 in Japanese Black cattle

Aduli Enoch Othniel MALAU-ADULI,[1] Tomomi NIIBAYASHI,[2] Takatoshi KOJIMA,[2] Kazunaga OSHIMA,[2] Yasushi MIZOGUCHI[3] and Masanori KOMATSU[1]

[1]National Institute of Livestock and Grassland Science, Tsukuba-shi, [2]National Agricultural Research Center for Western Region, Oda-shi and [3]Shirakawa Institute of Animal Genetics, Nishigo-mura, Fukushima-ken, Japan

ABSTRACT

The detection and mapping of segregating quantitative trait loci (QTL) that influence withers height, hip height, hip width, body length, chest width, chest depth, shoulder width, lumbar width, thurl width, pin bone width, rump length, cannon circumference, chest girth, abdominal width and abdominal girth at weaning was conducted on chromosomal regions of bovine chromosome one. The QTL analysis was performed by genotyping half-sib progeny of five Japanese Black sires using microsatellite DNA markers. Probability coefficients of inheriting allele 1 or 2 from the sire at specific chromosomal locations were computed. The phenotypic data of progeny were regressed on these probability coefficients in a within-common-parent regression analysis using a linear model that included fixed effects of sex, parity and season of birth, as well as age as a covariate. *F*-statistics were calculated every 1 cM on a linkage map. Permutation tests of 10 000 iterations were conducted to obtain chromosome-wide significance thresholds. A significant QTL for chest width was detected at 91 cM in family 3. The detection of this QTL boosts the prospects of implementing marker-assisted selection for body conformation traits in Japanese Black beef cattle.

KEYWORDS: beef cattle, body shape, conformation, Japanese Black, quantitative trait loci (QTL) mapping.

INTRODUCTION

Body shape and conformation measurements are useful selection traits in beef cattle because of their positive correlation with liveweight changes and growth (Varade & Ali 2001). In dairy cows, body size measurements are very useful in estimating body weight and productivity as demonstrated by the reports of Heinrichs *et al*. (1992), Enevoldsen and Kristensen (1997), Kertz *et al*. (1997) and Koenen and Groen (1998). In beef cattle, similar research has been conducted and reported by Gilbert *et al*. (1993), Vargas *et al*. (2000) and Magnabosco *et al*. (2002), but such information in Japanese Black cattle is scanty and limited to performance test and field carcass traits only (Mukai *et al*. 1995, 2000; Karnuah *et al*. 2001; Smith *et al*. 2001; Sosa *et al*. 2002). There is an abundance of published work on breed, age and sex differences in body measurements in cattle (Cestnik 2001; Rodriguez *et al*. 2001; Roy *et al*. 2001; Tozser *et al*. 2001; Afolayan *et al*. 2002a,b; Maiwashe *et al*. 2002). However, to our knowledge, apart from the work of Napolitano *et al*. (2001) with Italian Chianina ' Piemontese crossbred cattle and Ashwell *et al*. (1998) with US Holsteins, there is no published information on the detection of quantitative trait loci (QTL) for body measurements related to shape and conformation traits in any other

Correspondence: Aduli Enoch Othniel Malau-Aduli, School of Agricultural Science, University of Tasmania, Private Bag 54, Hobart, Tasmania 7001, Australia. (Email: Aduli.MalauAduli@utas.edu.au, aduli40@yahoo.co.uk)
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cattle breed. This justifies the need for the present study by our research into Japanese Black beef cattle.

The mapping of QTL is the first step towards identifying the genes and causal polymorphisms responsible for traits of importance in agriculture (Seaton *et al*. 2002). The detection of QTL influencing body shape and conformation traits would be useful in the implementation of marker-assisted selection in Japanese Black beef cattle. Comparative mammalian genomics reveal that bovine chromosome 1 (BTA1) is equivalent to the human chromosome 3 (http://bos.cvm.tamu.edu/htmls/rhbov1.html), which contains growth-regulating genes such as the growth hormone secretagogue receptor also known as *ghrelin* (Shuto *et al*. 2002; Hosoda *et al*. 2003), *glycogenin* (Mu *et al*. 2001) and *Pit-1* (Ohta *et al*. 1992; Hendriks-Stegeman *et al*. 2001). It is therefore justifiable to focus on BTA 1 in a scan for body conformation and growth-related QTL in Japanese Black cattle. Preliminary genome-wide scanning in our laboratory using only 30 animals (unpublished data) had suggested *Bos taurus* autosomes (BTA) 1, 2 and 5 as chromosomes containing segregating QTL that significantly influenced the growth traits in Japanese Black cattle. Therefore, in this confirmatory study with a larger data set of genotyped animals, we report for the first time, the association between microsatellite DNA markers and QTL on BTA1 influencing 15 body shape and conformation measurements at weaning in Japanese Black cattle.

MATERIALS AND METHODS

Animals and management

One hundred and thirty-two paternal half-sib progeny of five Japanese Black sires produced by artificial insemination at the Department of Livestock and Grassland Science, National Agricultural Research Center for Western Region, Oda, Shimane Prefecture, Japan, were genotyped. Sires 1 and 2 belonged to the line selected for increasing average daily gain and sires 3–5 belonged to the line selected for high beef marbling score. Routine management of the animals involved recording of weight at birth and monthly thereafter, until 18 months of age. Body shape and conformation measurements of withers height, hip height, hip width, body length, chest width, chest depth, shoulder width, lumbar width, thurl width, pin bone width, rump length, cannon circumference, chest girth, abdominal width and abdominal girth were also taken monthly. Calves were allowed to suckle their dams in addition to being fed 1.5 kg/day per head of concentrate and 1 kg/day per head of corn silage until 5 months of age when they were weaned. After weaning, they were moved to the grower's barn and continued to be raised on concentrates (37% corn grain, 39% rice bran, 17% soybean meal, 7% minerals) and corn silage until 10 months of age. Between 10 and 18 months of age, they were moved to another barn and fed intensively. The proportions of the ration on a dry matter basis were 61% corn grain, 34% soybean and corn glutein meal, 2% bran and 3% minerals. For every 20 kg bag, this ration provided an estimated 21% crude protein, 3.5% crude fat, 5% crude fiber, 7% ash, 0.6% calcium, 0.40% phosphate and a total digestible nutrients of 77%. From 18 to 24 months of age, breeding females were returned to the calving barn and the steers were moved to the fattening barn where they were raised primarily on "Mosa meal" a specially formulated fattening ration containing 77% corn and rye grain, 10.5% wheat and rice bran, 9% soybean oil meal and 3.5% mineral supplement. At all ages, routine veterinary vaccinations and health checks were performed.

Extraction of genomic DNA

Following the method of Sambrook *et al*. (1989) and described in detail elsewhere (Malau-Aduli *et al*. 2003), genomic DNA was extracted and prepared from blood leukocytes and sperm.

Polymerase chain reaction (PCR)

The PCR premix (13 μL) comprised: 10.55 μL of distilled water, 1.04 μL of 2.5 mmol/L dNTP mixture (Takara, Shiga, Japan), 1.3 μL of 10 ′ buffer containing 15 mmol/L $MgCl_2$ and 0.11 μL of 25 mmol/L of $MgCl_2$. A primer (12.5 pmol/μL) of the microsatellite DNA markers, each of which was labeled with one of three different fluorescent labels, FAM, HEX and TET (supplied by the Shirakawa Institute of Animal Genetics, Fukushima, Japan, and based on the bovine genetic map at the US Meat Animal Research Center (Kappes *et al*. 1997; http://sol.marc.usda.gov)) was added to the PCR premix. Genomic DNA (1 μL; 20 ng/μL) was added, followed by 0.5 μL of Taq polymerase enzyme (0.75 units/μL) containing 50% glycerol (Takara). The PCR plates were hotplate-sealed and subjected to PCR in a DNA thermal cycler. The annealing temperature settings were 50°C, 55°C and 60°C.

Genotyping

Prior to genotyping, the PCR products were mixed with the markers, which could be genotyped simultaneously in combinations of 4 μL of HEX, 1 μL of FAM and 1 μL of TET, for multiplex genotyping. Next, 0.8 μL of the mixed PCR products was added to 4.5 μL of DNA size marker, centrifuged for 1 min at 120 *g* and denatured using the PCR machine at a denaturing temperature of 94°C for 9 min. The denatured products were subjected to electrophoresis and genotyping in an automated ABI 377 DNA Sequencer. The number of informative microsatellite DNA markers used for the genotyping in each family is shown in Table 1.

Traits analyzed

Offspring of the five sires born between 1997 and 2002 were evaluated (SAS Institute 2002) for the following body shape and conformation measurements at weaning (5 months of age): withers height, hip height, hip width, body length, chest width, chest depth, shoulder width, lumbar width, thurl width, pin bone width, rump length, cannon circumference, chest girth, abdominal width and abdominal girth.

QTL analysis

We adopted the methods of Haley and Knott (1992), Knott *et al*. (1996) and de Koning *et al*. (1998, 2001) for the detection and mapping of QTL in half-sib populations using least squares simple regression. We used the *QTL Express* computer program with a web-based user interface (http://qtl.cap.ed.ac.uk/) developed by Seaton *et al*. (2002) and based on the methods of the previously mentioned researchers for the QTL analysis. The half-sib model of *QTL Express* run within and across sires, implemented the analysis in a two-step procedure. First, microsatellite DNA marker data on progeny and their common parent (sire) were combined in a multipoint approach to calculate the probabilities of inheriting allele 1 or 2 from the sire at specific chromosomal intervals. These probabilities were combined into coefficients with values between 0.0 and 1.0. Second, the phenotypic data on progeny were regressed on these probability coefficients in a within-common-parent regression analysis. A linear model containing the fixed effects of sire, sex, parity and season of birth as well as age as a covariate, was fitted to the coefficients and phenotypic data. Appropriate F-statistic thresholds for a $P < 0.05$ chromosome-wise type 1 error rate were generated by permutation test of 10 000 iterations as described by Churchill and Doerge (1994), Doerge and Churchill (1996) (and applied to other half-sib studies by Spelman *et al*. 1996 and Vilkki *et al*. 1997). In determining significant thresholds, the *QTL Express* software (Seaton *et al*. 2002) computed both the *F*-statistic and the *F*-threshold at $P < 0.05$ chromosome-wise level. QTL were classified as significant when the *F*-statistic exceeded the *F*-threshold, indicating a marker-trait association.

RESULTS

The means and standard deviations of the body conformation measurements at weaning in the five Japanese Black families are shown in Table 2. It was evident that in all families, almost all of the body conformation measurements within traits were similar. The only clearly visible sign of significant differences between families was in the chest girth (CHESTGTH) measurements, which were higher in families 1 and 2 (125.9 and 127.2 cm, respectively) than in families 3–5 (121.7, 123.4 and 120.2 cm, respectively). Table 1 shows the microsatellite DNA markers that were utilized in genotyping the sires and half-sib progeny and their relative positions on the BTA1 map; 18, 23, 11, 19 and 17 markers were informative for families 1, 2, 3, 4 and 5, respectively.

The estimates of allele substitution of sire QTL effects and locations obtained at the peak of the *F*-statistics and thresholds of chromosome-wide 5% significant levels for body shape and conformation traits in the five Japanese Black families are shown in Table 3, and the plot of the *F*-statistics in groups of five body conformation measurements is shown in Fig. 1. A significant QTL for chest width (CHESTWD) at 91 cM was detected in family 3.

DISCUSSION

Animal improvement has been achieved by selection based on either phenotype or the predicted additive genetic merit of superior animals for production traits. Molecular biology techniques allow the identification of genetic variation at specific loci and the association between QTL and production traits. The final goal is to use marker-assisted selection to improve the genetic gain achieved by selection as a result of higher accuracy on the estimation of an animal's genetic value (Tambasco *et al*. 2003). Microsatellites are thought to be the best genome markers and useful ones can be included in marker-assisted selection programs

Table 1 Microsatellite DNA markers used for genotyping the five Japanese Black cattle families and their relative positions on the map (cM)*

Family	Marker	Position	Family	Marker	Position	Family	Marker	Position	Family	Marker	Position	Family	Marker	Position
1	BMS1928	6.9	2	BM8139	8.2	3	BMS2321	14.0	4	BMS1928	6.9	5	BM8139	8.2
1	BMS711	21.3	2	TGLA57	46.2	3	ILSTS104	28.2	4	BMS711	21.3	5	BMS2321	14.0
1	ILSTS104	28.2	2	BMS4012	51.0	3	BMS4002	47.9	4	TGLA57	46.2	5	BMS711	21.3
1	MB055	32.0	2	BMS4013	61.3	3	BMS4012	51.0	4	BMS4035	55.0	5	BMS2725	41.8
1	TGLA57	46.2	2	BMS4001	64.7	3	BMS4035	55.0	4	BMS4029	61.3	5	BMS4002	47.9
1	BMS4012	51.0	2	BM9019	67.5	3	RME36	63.0	4	BM9019	67.5	5	BMS4012	51.0
1	BMS4035	55.0	2	BL26–1	77.7	3	BM8246	76.2	4	BMS4008	71.7	5	RM326	55.6
1	RM326	55.6	2	BMS4006	79.4	3	BMS119	88.6	4	BMS4048	76.2	5	BMS4030	59.2
1	RME36	63.0	2	URB038	80.6	3	BMS4019	98.8	4	URB038	80.6	5	BMS4029	61.3
1	INRA049	67.5	2	MCM130	83.3	3	UWCA46	113.8	4	BMS4010	87.1	5	INRA119	68.7
1	BM65O6	69.2	2	BMS4010	87.1	3	BMS599	125.8	4	BM864	88.2	5	BMS4008	71.7
1	URB038	80.6	2	BM864	88.2				4	BMS1170	92.8	5	BM8246	76.2
1	BMS4052	94.6	2	BMS1170	92.8				4	BMS4019	98.8	5	BMS4006	79.4
1	BMS4028	95.6	2	BMS4028	95.6				4	BMS4011	102.1	5	BMS4010	87.1
1	BMS4040	98.8	2	BMS4019	98.8				4	BMS4049	114.3	5	BMS4019	98.8
1	BMS1789	100.9	2	BMS1789	100.9				4	BMS918	118.1	5	BMS1757	108.3
1	BMS4044	128.7	2	BMS1939	104.1				4	BMS599	125.8	5	BMS4044	128.7
1	BMS2263	135.1	2	BMS4039	108.3				4	BMS4044	128.7			
			2	BM3205	113.8				4	BMS922	135.5			
			2	BMS5993	125.8									
			2	BMS404	128.7									
			2	BMS2263	135.1									
			2	BMS4014	135.5									
Total	18			23			11			19			17	

*Based on the bovine genetic map at the US Meat Animal Research Center (Kappes *et al.* 1997; http://sol.marc.usda.gov).

Table 2 Body conformation measurements at weaning (means ± SD; cm) of the progeny of the five Japanese Black sires

Trait	Family 1	Family 2	Family 3	Family 4	Family 5
Withers height	99.5 ± 3.9	100.9 ± 3.5	98.5 ± 3.5	97.5 ± 2.7	97.6 ± 4.0
Hip height	103.1 ± 3.9	103.0 ± 3.0	101.0 ± 3.8	101.1 ± 3.8	98.7 ± 4.1
Body length	106.5 ± 5.9	108.1 ± 5.0	103.2 ± 7.5	103.2 ± 4.5	101.9 ± 5.3
Chest width	28.1 ± 2.2	29.5 ± 2.3	27.7 ± 2.6	26.9 ± 2.2	27.2 ± 1.6
Shoulder width	31.2 ± 2.6	31.4 ± 2.1	28.4 ± 2.2	28.6 ± 2.0	27.4 ± 2.3
Chest depth	46.3 ± 1.8	46.6 ± 1.5	44.7 ± 1.8	45.5 ± 1.4	43.8 ± 2.2
Hip width	28.3 ± 1.8	29.0 ± 1.3	26.3 ± 2.1	28.1 ± 1.4	27.4 ± 1.5
Lumbar width	22.7 ± 1.5	23.1 ± 1.0	21.1 ± 2.1	22.6 ± 1.3	22.0 ± 1.3
Thurl width	33.0 ± 2.2	33.6 ± 1.7	31.0 ± 1.6	31.3 ± 1.9	31.0 ± 2.0
Pin bone width	20.5 ± 2.1	20.6 ± 1.3	18.6 ± 1.9	18.9 ± 1.0	18.1 ± 1.4
Rump length	35.2 ± 2.1	35.8 ± 1.8	34.6 ± 1.7	35.3 ± 1.4	34.4 ± 1.7
Cannon circumference	14.4 ± 0.9	14.7 ± 0.9	13.8 ± 1.0	13.5 ± 0.8	13.4 ± 0.9
Chest girth	125.9 ± 5.2[a]	127.2 ± 4.3[a]	121.7 ± 4.9[b]	123.4 ± 3.8[b]	120.2 ± 5.9[b]
Abdominal width	37.0 ± 2.5	37.7 ± 2.5	35.4 ± 2.9	36.5 ± 2.2	35.5 ± 1.9
Abdominal girth	144.0 ± 7.0	143.5 ± 6.1	138.5 ± 7.4	140.6.0 ± 6	138.0 ± 7.2
No. of progeny	40	36	19	17	20

Means in rows bearing different superscripts significantly differ between families.

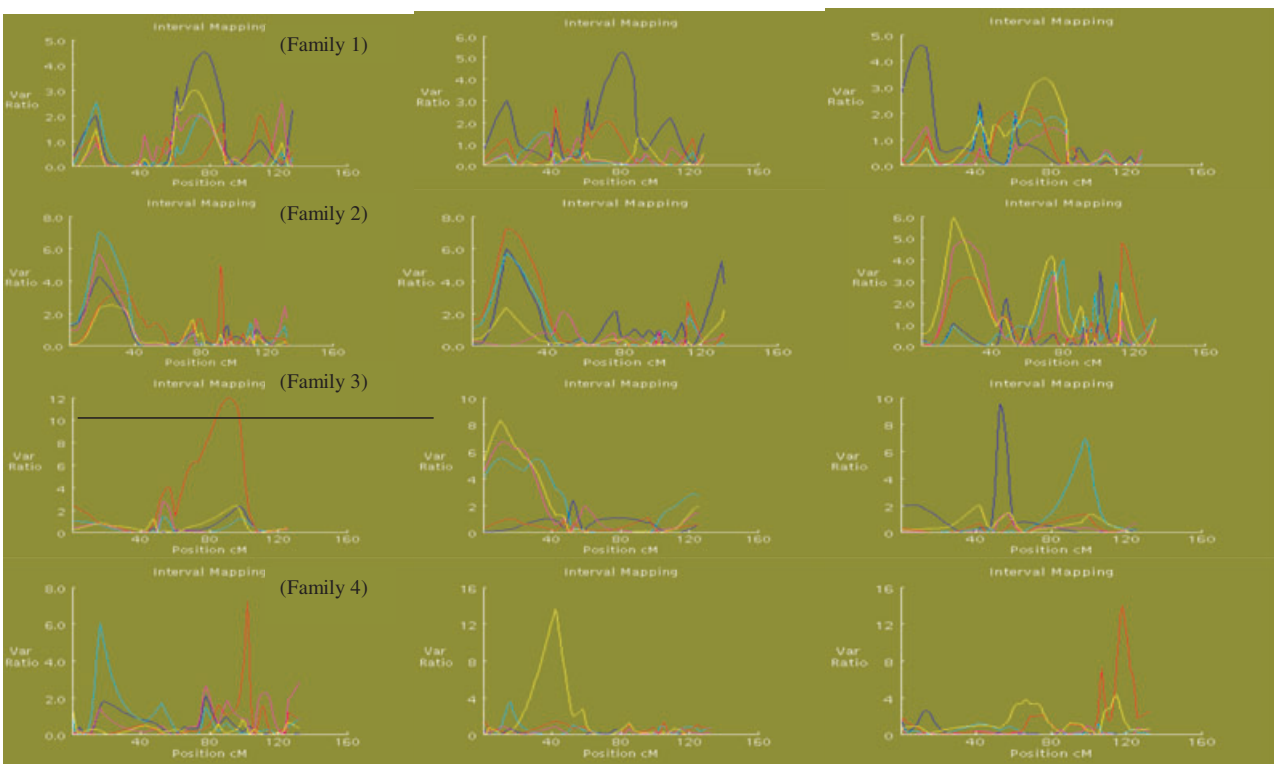

Fig. 1 Map of the *F*-statistics depicting the positions of quantitative trait loci (QTL) of body conformation traits in Japanese Black cattle. A QTL for CHESTWD at 91 cM reached chromosome-wide significance ($P < 0.05$) in family 3 only (threshold in bold).

to increase the rate of genetic progress (Georges *et al.* 1993). Napolitano *et al.* (1996) reported the localization of three microsatellites, IDVGA-2, IDVGA-3 and IDVGA-46, on bovine chromosomes 2, 11 and 19, respectively, and their association with beef performance traits in F1 Piemontese Chianina crossbred cows. Of the three microsatellites, IDVGA-46 was reported to be the best marker for most

Table 3 Allele substitution/sire QTL effects (β ± SE) and estimated QTL locations (cM) for body shape and conformation traits in the five Japanese Black cattle families

Trait	Family 1	Family 2	Family 3	Family 4	Family 5
WHT					
β ± SE	−3.5 ± 1.7	2.8 ± 1.3	5.5 ± 3.6	2.5 ± 1.7	−4.6 ± 1.7
QTL (cM)	77 (*F* = 4.5/9.0) NS	18 (*F* = 4.3/9.0) NS	97 (*F* = 2.3/12.8) NS	78 (*F* = 2.1/44.6) NS	58 (*F* = 7.5/15.1) NS
HIPHT					
β ± SE	−2.5 ± 1.6	3.0 ± 1.1	−2.9 ± 2.4	−4.2 ± 1.7	3.2 ± 1.7
QTL (cM)	14 (*F* = 2.5/9.4) NS	18 (*F* = 7.0/9.0) NS	53 (*F* = 1.4/11.9) NS	16 (*F* = 6.1/76.0) NS	0 (*F* = 3.7/13.0) NS
BL					
β ± SE	3.9 ± 2.4	4.7 ± 2.0	−7.1 ± 4.3	−10.8 ± 6.4	−5.4 ± 2.8
QTL (cM)	122 (*F* = 2.6/8.9) NS	18 (*F* = 5.7/9.2) NS	53 (*F* = 2.8/12.9) NS	132 (*F* = 2.8/87.5) NS	71 (*F* = 3.7/16.2) NS
CHESTWD					
β ± SE	−1.2 ± 0.8	−2.0 ± 0.9	5.3 ± 1.5	−7.9 ± 2.9	−1.1 ± 0.9
QTL (cM)	109 (*F* = 2.0/9.3) NS	92 (*F* = 5.0/9.3) NS	91 (*F* = 12.0/10.05) significant	102 (*F* = 7.2/93.9) NS	5 (*F* = 1.2/14.8) NS
SHOUWD					
β ± SE	−2.0 ± 1.1	1.4 ± 0.9	2.5 ± 1.6	−3.7 ± 3.1	−2.0 ± 1.1
QTL (cM)	71 (*F* = 3.0/8.9) NS	25 (*F* = 2.5/9.7) NS	95 (*F* = 2.4/12.4) NS	0 (*F* = 1.4/95.4) NS	72 (*F* = 3.1/13.8) NS
CHESTDP					
β ± SE	−2.1 ± 0.9	1.4 ± 0.6	−1.5 ± 0.9	−1.5 ± 1.6	3.4 ± 1.7
QTL (cM)	81 (*F* = 5.3/9.4) NS	18 (*F* = 6.0/10.2) NS	52 (*F* = 2.4/11.5) NS	0 (*F* = 0.8/74.5) NS	120 (*F* = 3.9/13.3) NS
HIPWDT					
β ± SE	1.2 ± 1.0	1.1 ± 0.5	1.8 ± 0.8	−2.0 ± 1.1	−0.9 ± 0.6
QTL (cM)	36 (*F* = 1.6/9.8) NS	18 (*F* = 5.7/10.3) NS	10 (*F* = 5.5/13.2) NS	16 (*F* = 3.5/39.9) NS	72 (*F* = 2.1/10.8) NS
LUMBARWD					
β ± SE	0.8 ± 0.7	−0.6 ± 0.4	1.8 ± 0.7	0.4 ± 0.5	−0.8 ± 0.7
QTL (cM)	38 (*F* = 1.4/8.9) NS	48 (*F* = 2.1/9.2) NS	11 (*F* = 6.8/12.3) NS	42 (*F* = 0.9/49.5) NS	72 (*F* = 1.6/14.6) NS
THURLWD					
β ± SE	−1.4 ± 0.9	1.9 ± 0.7	1.2 ± 1.2	1.0 ± 0.8	−0.8 ± 0.7
QTL (cM)	42 (*F* = 2.7/9.1) NS	18(*F* = 7.3/9.3) NS	95 (*F* = 1.1/12.2) NS	42 (*F* = 1.5/66.9) NS	71 (*F* = 1.3/15.0) NS
PINBWD					
β ± SE	1.2 ± 1.1	0.8 ± 0.5	2.6 ± 0.9	1.5 ± 0.4	−1.9 ± 1.0
QTL (cM)	91 (*F* = 1.3/9.2) NS	18 (*F* = 2.3/9.2) NS	10 (*F* = 8.3/11.4) NS	42 (*F* = 13.7/52.3) NS	101 (*F* = 3.8/14.9) NS
RUMPL					
β ± SE	−2.2 ± 1.0	1.0 ± 0.6	−1.7 ± 0.5	−1.8 ± 1.1	−1.4 ± 0.6
QTL (cM)	11 (*F* = 4.6/8.9) NS	101 (*F* = 3.5/9.9) NS	53 (*F* = 9.5/10.9) NS	13 (*F* = 2.7/32.5) NS	72 (*F* = 5.0/12.4) NS
CANNONCIR					
β ± SE	−0.4 ± 0.3	−0.5 ± 0.2	1.7 ± 0.7	0.4 ± 0.4	−0.2 ± 0.3
QTL (cM)	42 (*F* = 2.1/9.4) NS	80 (*F* = 4.0/9.5) NS	98 (*F* = 6.9/11.5) NS	42 (*F* = 1.2/57.0) NS	53 (*F* = 0.4/14.3) NS
CHESTGTH					
β ± SE	−2.8 ± 2.3	3.8 ± 1.7	−4.2 ± 3.6	−4.6 ± 4.7	−3.9 ± 3.0
QTL (cM)	14 (*F* = 1.5/9.1) NS	24 (*F* = 4.9/9.9) NS	56 (*F* = 1.4/12.9) NS	99 (*F* = 1.0/69.6) NS	71 (*F* = 1.8/14.4) NS
ABDWD					
β ± SE	−1.9 ± 1.3	2.2 ± 1.0	2.8 ± 2.4	−5.2 ± 1.4	−1.3 ± 1.0
QTL (cM)	70 (*F* = 2.2/8.9) NS	113 (*F* = 4.8/10.2) NS	97 (*F* = 1.4/13.6) NS	118 (*F* = 14.0/60.2) NS	3 (*F* = 1.5/15.9) NS
ABDGTH					
β ± SE	−6.3 ± 3.4	6.0 ± 2.5	−5.1 ± 3.5	−13.2 ± 6.3	−2.4 ± 3.8
QTL (cM)	77 (*F* = 3.3/9.2) NS	18 (*F* = 6.0/9.5) NS	42 (*F* = 2.1/12.3) NS	115 (*F* = 4.3/97.6) NS	56 (*F* = 0.4/15.5) NS

Figures in brackets are *F*-statistic/*F*-threshold values at $P < 0.05$ chromosome-wide level

WHT, withers height; HIPHT, hip height; BL, body length; CHESTWD, chest width; SHOUWD, shoulder width; CHESTDP, chest depth; HIPWDT, hip width; LUMBARWD, lumbar width; THURLWD, thurl width; PINBWD, pin bone width; RUMPL, rump length; CANNONCIR, cannon circumference; CHESTGTH, chest girth; ABDWD, abdominal width; ABDGTH, abdomnal girth; NS, not significant.

conformational traits in this crossbred population, and that animals homozygous for allele 205 gave the best results in terms of linkage with the segregating QTL for beef conformation (Napolitano *et al*. 2001). Their study examined only seven body conformation measurements: withers height, body length, chest width, chest depth, chest girth, rump length and pelvis width, whereas we examined 15 measurements and detected a significant QTL for CHESTWD located at 91 cM. The implication is that the microsatellite markers BMS119 and BMS4019 flanking this interval can be used in marker-assisted selection to introduce or retain the beneficial QTL allele. The phenomenon of genetic linkage means that each marker can be used to follow the inheritance of a section of the linked chromosome. However, markers have to be very closely linked to the causative mutation in the trait gene if they are to remain associated with specific QTL alleles through several generations of selection and therefore be useful in practical breeding programs. If a genetic marker and a trait are significantly linked, as portrayed in our study, there is a tendency for such associations to be maintained at a population level. This phenomenon of linkage disequilibrium could be exploited to locate the trait genes using single nucleotide polymorphisms (SNP), which is when two DNA sequences differ by a single base. There is ongoing work in our laboratory to confirm or dispute the presence of significant QTL for body conformation and growth on BTA2 and BTA5. It is our goal to utilize positional cloning using the candidate gene approach to identify the underlying mutation linked to the QTL detected in the present study.

There were significant differences between families in CHESTGTH measurements, for which families 1 and 2 were had higher results than families 3–5, which was not entirely surprising because sires 1 and 2 had been selected for average daily gain (daily gain line) whereas sires 3–5 belonged to the beef marbling score line. Chest girth is an important body conformation measurement that has been reported in Japanese Black cattle. Mukai *et al*. (1995) studied the genetic relationships between body measurements, growth and field carcass performance traits and reported highly significant and positive genetic correlations between CHESTGTH and carcass weight at the beginning, middle and end of performance testing of 0.64, 0.77 and 0.79, respectively. They concluded that it was possible to improve total merit of the carcass by introducing CHESTGTH into performance testing of Japanese Black cattle. Other studies (Oyama *et al*. 1996; Kitamura *et al*. 1999) on genetic relationships among recorded body measurement traits, reproductive traits of breeding females and carcass traits in Japanese Black cattle buttress the finding of Mukai *et al*. (1995) that there is an unfavorable or low correlation between CHESTGTH and beef marbling score (–0.07, 0.28 and 0.21 at the beginning, middle and end of performance testing, respectively). It is this low correlation that was also observed in this present study with the beef marbling score families having lower CHESTGTH measurements than the daily gain line families. Other body conformation measurements, such as chest depth, thurl width and withers height, were also found to be genetically correlated with field carcass weight, ranging from 0.64 to 0.90 (Mukai *et al*. 1995), indicating that body conformation measurements can be valuable in selection for meat quality as well. Unpublished data from our group show a significant and positive relationship between body conformation measurements and average daily gain to weaning and yearling age. Thus, the identification of a significant QTL for CHESTWD in the present study gives hope for the utilization of markers closely linked to this trait for the implementation of marker-assisted selection for growth and carcass traits.

In conclusion, the presence of a QTL on BTA1 located at 91 cM between the markers BMS119 and BMS4019 significantly segregating for CHESTWD in Japanese Black cattle has been demonstrated. The detection of this significant QTL boosts the prospect of implementing marker-assisted selection for body conformation traits in the breed. Furthermore, this finding could pave the way for positional cloning using candidate genes in Japanese Black cattle such as *ghrelin*, *glycogenin* or *Pit-1*. The prospect of subsequently isolating and characterizing the genes using single nucleotide polymorphisms (SNP) appears promising.

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